

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 5, 2006, 18:11:35 ; Search time 200 Seconds
(without alignments)
857.281 Million cell updates/sec

Title: US-10-092-934-10
Perfect score: 2034
Sequence: 1 MEFSLLLPRLECNGAISAHR.....FIRGGVSPYLSGWSQTPDLR 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2034	100.0	375	3	AAB01399	Aab01399 Neuron-as
2	2034	100.0	375	5	ABB81538	Abb81538 Neural th
3	2034	100.0	375	5	AAE29142	Aae29142 AD7c-NTP
4	2034	100.0	375	6	ABR63268	Abr63268 AD7c-NTP
5	2034	100.0	375	6	ADA84017	Ada84017 Human POM
6	2034	100.0	375	6	ABU03024	Abu03024 Human neu
7	2034	100.0	375	6	ABB99774	Abb99774 Amino aci
8	2034	100.0	375	6	ABJ19445	Abj19445 AD7C-neur
9	2034	100.0	375	7	ADB37642	Adb37642 Human neu
10	2034	100.0	375	8	ADR14409	Adr14409 Human NF-
11	2034	100.0	375	9	AEA30020	Aea30020 Human neu
12	1415.5	69.6	397	2	AAR95913	Aar95913 Neural th
13	928	45.6	381	4	AAU30235	Aau30235 Novel hum
14	927.5	45.6	382	4	AAU32610	Aau32610 Novel hum
15	927.5	45.6	382	4	AAU31818	Aau31818 Novel hum
16	927.5	45.6	382	4	AAU32707	Aau32707 Novel hum

17	849	41.7	324	4	AAU29573	Aau29573	Novel	hum
18	849	41.7	324	4	AAU29579	Aau29579	Novel	hum
19	822.5	40.4	411	4	ABG08428	Abg08428	Novel	hum
20	739	36.3	317	4	AAU33200	Aau33200	Novel	hum
21	735	36.1	290	4	ABG21913	Abg21913	Novel	hum
22	734.5	36.1	361	5	ABG68738	Abg68738	Human	pro
23	729	35.8	449	5	ABJ01057	Abj01057	Ovary	cel
24	701.5	34.5	332	5	ADK34410	Adk34410	Novel	hum
25	609	29.9	257	4	AAO10294	Aao10294	Human	pol
26	590	29.0	276	4	ABG07919	Abg07919	Novel	hum
27	575	28.3	302	5	ADK36936	Adk36936	Novel	hum
28	574	28.2	185	4	AAO06014	Aao06014	Human	pol
29	569	28.0	241	4	ABB11464	Abb11464	Human	neu
30	567.5	27.9	196	7	ADE09985	Ade09985	Novel	pro
31	563	27.7	202	4	AAU30686	Aau30686	Novel	hum
32	561	27.6	250	4	AAU31823	Aau31823	Novel	hum
33	561	27.6	250	7	ADE09441	Ade09441	Novel	pro
34	560	27.5	296	4	AAU33304	Aau33304	Novel	hum
35	554.5	27.3	232	5	ADK36978	Adk36978	Novel	hum
36	553	27.2	175	4	AAU31782	Aau31782	Novel	hum
37	550.5	27.1	215	4	AAU31513	Aau31513	Novel	hum
38	546	26.8	215	4	ABG07921	Abg07921	Novel	hum
39	543.5	26.7	216	4	AAU32615	Aau32615	Novel	hum
40	524	25.8	304	4	AAU30391	Aau30391	Novel	hum
41	522.5	25.7	175	4	AAU31857	Aau31857	Novel	hum
42	521.5	25.6	418	4	AAU31980	Aau31980	Novel	hum
43	520	25.6	396	4	AAU30455	Aau30455	Novel	hum
44	517	25.4	213	4	AAM25396	Aam25396	Human	pro
45	504.5	24.8	196	4	AAU31786	Aau31786	Novel	hum

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OM protein - protein search, using sw model

Run on: June 5, 2006, 18:29:46 ; Search time 50 Seconds
(without alignments)
656.480 Million cell updates/sec

Title: US-10-092-934-10
Perfect score: 2034
Sequence: 1 MEFSLLLPRLECNGAISAHR.....FIRGGVSPYLSGWSQTPDLR 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2034	100.0	375	1	US-08-454-557C-121	Sequence 121, App
2	2034	100.0	375	1	US-08-340-426D-121	Sequence 121, App
3	2034	100.0	375	1	US-08-450-673C-121	Sequence 121, App
4	2034	100.0	375	2	US-09-872-968-2	Sequence 2, Appli
5	2034	100.0	375	2	US-10-153-334-1	Sequence 1, Appli
6	1415.5	69.6	397	5	PCT-US95-17111A-121	Sequence 121, App
7	377.5	18.6	158	2	US-10-104-047-3047	Sequence 3047, Ap
8	324	15.9	189	2	US-10-104-047-3196	Sequence 3196, Ap
9	310	15.2	101	2	US-10-094-749-2181	Sequence 2181, Ap
10	307	15.1	114	2	US-10-104-047-2423	Sequence 2423, Ap
11	301	14.8	156	2	US-10-104-047-2334	Sequence 2334, Ap
12	299.5	14.7	176	2	US-10-094-749-2950	Sequence 2950, Ap
13	283.5	13.9	110	2	US-10-104-047-3422	Sequence 3422, Ap
14	283	13.9	123	2	US-10-104-047-2112	Sequence 2112, Ap
15	280	13.8	152	2	US-10-104-047-2372	Sequence 2372, Ap
16	267.5	13.2	96	2	US-09-513-999C-6065	Sequence 6065, Ap
17	262	12.9	46	2	US-10-153-334-48	Sequence 48, Appl
18	261.5	12.9	128	2	US-10-104-047-2789	Sequence 2789, Ap
19	259.5	12.8	144	2	US-09-513-999C-6953	Sequence 6953, Ap

20	258	12.7	129	2	US-10-104-047-2565	Sequence 2565, Ap
21	256	12.6	108	2	US-09-513-999C-7878	Sequence 7878, Ap
22	254.5	12.5	239	2	US-09-800-729-193	Sequence 193, App
23	254.5	12.5	310	2	US-09-800-729-190	Sequence 190, App
24	253	12.4	118	2	US-09-663-600A-114	Sequence 114, App
25	252.5	12.4	110	2	US-10-104-047-2974	Sequence 2974, Ap
26	251.5	12.4	113	2	US-10-094-749-2649	Sequence 2649, Ap
27	251	12.3	776	2	US-10-020-079-24	Sequence 24, Appl
28	251	12.3	776	2	US-10-413-437-24	Sequence 24, Appl
29	251	12.3	789	2	US-10-020-079-22	Sequence 22, Appl
30	251	12.3	789	2	US-10-413-437-22	Sequence 22, Appl
31	251	12.3	863	2	US-10-020-079-32	Sequence 32, Appl
32	251	12.3	863	2	US-10-413-437-32	Sequence 32, Appl
33	251	12.3	876	2	US-10-020-079-30	Sequence 30, Appl
34	251	12.3	876	2	US-10-413-437-30	Sequence 30, Appl
35	251	12.3	889	2	US-10-020-079-20	Sequence 20, Appl
36	251	12.3	889	2	US-10-413-437-20	Sequence 20, Appl
37	251	12.3	895	2	US-10-020-079-18	Sequence 18, Appl
38	251	12.3	895	2	US-10-413-437-18	Sequence 18, Appl
39	251	12.3	976	2	US-10-020-079-28	Sequence 28, Appl
40	251	12.3	976	2	US-10-413-437-28	Sequence 28, Appl
41	251	12.3	982	2	US-10-020-079-26	Sequence 26, Appl
42	251	12.3	982	2	US-10-413-437-26	Sequence 26, Appl
43	250	12.3	97	2	US-09-513-999C-4770	Sequence 4770, Ap
44	250	12.3	100	2	US-10-094-749-3044	Sequence 3044, Ap
45	250	12.3	132	2	US-09-636-215-573	Sequence 573, App

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OM protein - protein search, using sw model

Run on: June 5, 2006, 18:41:47 ; Search time 185 Seconds
(without alignments)
938.949 Million cell updates/sec

Title: US-10-092-934-10
Perfect score: 2034
Sequence: 1 MEFSLLLPRLECNGAISAHR.....FIRGGVSPYLSGWSQTPDLR 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2034	100.0	375	3	US-09-964-666-2
2	2034	100.0	375	3	US-09-964-412-2
3	2034	100.0	375	3	US-09-964-667-2
4	2034	100.0	375	3	US-09-872-968-2
5	2034	100.0	375	3	US-09-964-678A-2
6	2034	100.0	375	4	US-10-146-130-2
7	2034	100.0	375	4	US-10-092-934-10
8	2034	100.0	375	4	US-10-153-334-1
9	2034	100.0	375	4	US-10-198-069-1
10	2034	100.0	375	4	US-10-157-031-299
11	2034	100.0	375	4	US-10-198-070-1
12	2034	100.0	375	4	US-10-755-889-410
13	2034	100.0	375	5	US-10-910-173-2
14	822.5	40.4	411	5	US-10-450-763-38787
15	735	36.1	290	5	US-10-450-763-52272
16	734.5	36.1	361	3	US-09-995-494-107
17	729	35.8	449	4	US-10-007-280A-140
18	590	29.0	276	5	US-10-450-763-38278
19	569	28.0	241	4	US-10-276-774-1834
20	546	26.8	215	5	US-10-450-763-38280

21	517	25.4	213	4	US-10-296-115-911	Sequence 911, App
22	471	23.2	286	4	US-10-291-172-654	Sequence 654, App
23	471	23.2	286	4	US-10-221-278-654	Sequence 654, App
24	464	22.8	154	5	US-10-450-763-38784	Sequence 38784, A
25	457.5	22.5	264	5	US-10-450-763-52437	Sequence 52437, A
26	428.5	21.1	183	3	US-09-989-920-245	Sequence 245, App
27	427	21.0	146	5	US-10-450-763-38554	Sequence 38554, A
28	407	20.0	361	4	US-10-276-774-1862	Sequence 1862, Ap
29	382.5	18.8	341	5	US-10-220-335-586	Sequence 586, App
30	382.5	18.8	673	4	US-10-157-031-291	Sequence 291, App
31	377.5	18.6	158	4	US-10-104-047-3047	Sequence 3047, Ap
32	377.5	18.6	158	6	US-11-072-512-3047	Sequence 3047, Ap
33	365.5	18.0	126	5	US-10-450-763-38786	Sequence 38786, A
34	356.5	17.5	603	4	US-10-408-765A-140	Sequence 140, App
35	353.5	17.4	217	4	US-10-017-161-1956	Sequence 1956, Ap
36	353.5	17.4	217	4	US-10-292-798-1604	Sequence 1604, Ap
37	349	17.2	157	4	US-10-108-260A-4272	Sequence 4272, Ap
38	336	16.5	148	4	US-10-276-774-1784	Sequence 1784, Ap
39	332	16.3	108	4	US-10-078-090-143	Sequence 143, App
40	328.5	16.2	252	5	US-10-450-763-33745	Sequence 33745, A
41	324	15.9	189	4	US-10-104-047-3196	Sequence 3196, Ap
42	324	15.9	189	6	US-11-072-512-3196	Sequence 3196, Ap
43	317	15.6	122	5	US-10-450-763-38275	Sequence 38275, A
44	316	15.5	152	4	US-10-198-070-112	Sequence 112, App
45	311	15.3	74	4	US-10-276-774-1929	Sequence 1929, Ap

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OM protein - protein search, using sw model

Run on: June 5, 2006, 18:42:11 ; Search time 16 Seconds
(without alignments)
271.058 Million cell updates/sec

Title: US-10-092-934-10
Perfect score: 2034
Sequence: 1 MEFSLLLPRLECNGAISAHR.....FIRGGVSPYLSGWSQTPDLR 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 58871 seqs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	349	17.2	157	7	US-11-293-697-4272	Sequence 4272, Ap
2	303	14.9	203	7	US-11-293-697-2748	Sequence 2748, Ap
3	290.5	14.3	127	7	US-11-293-697-2558	Sequence 2558, Ap
4	287	14.1	180	7	US-11-293-697-4793	Sequence 4793, Ap
5	274	13.5	125	7	US-11-293-697-4066	Sequence 4066, Ap
6	262.5	12.9	100	7	US-11-293-697-3143	Sequence 3143, Ap
7	262.5	12.9	179	7	US-11-293-697-4646	Sequence 4646, Ap
8	261	12.8	140	7	US-11-293-697-2547	Sequence 2547, Ap
9	260.5	12.8	273	7	US-11-293-697-2884	Sequence 2884, Ap
10	258.5	12.7	140	7	US-11-293-697-4151	Sequence 4151, Ap
11	257	12.6	134	7	US-11-293-697-4651	Sequence 4651, Ap
12	256	12.6	138	7	US-11-293-697-4194	Sequence 4194, Ap
13	252.5	12.4	108	7	US-11-293-697-4789	Sequence 4789, Ap
14	249	12.2	116	7	US-11-293-697-2525	Sequence 2525, Ap
15	248	12.2	440	6	US-10-196-749-386	Sequence 386, App
16	248	12.2	440	7	US-11-101-316-134	Sequence 134, App
17	247.5	12.2	630	7	US-11-293-697-4498	Sequence 4498, Ap
18	242.5	11.9	204	7	US-11-293-697-3687	Sequence 3687, Ap

19	240	11.8	216	7	US-11-293-697-4836	Sequence 4836, Ap
20	239	11.8	105	7	US-11-293-697-3988	Sequence 3988, Ap
21	233.5	11.5	129	7	US-11-293-697-2565	Sequence 2565, Ap
22	230.5	11.3	108	7	US-11-293-697-3308	Sequence 3308, Ap
23	229.5	11.3	118	7	US-11-293-697-4243	Sequence 4243, Ap
24	222	10.9	114	7	US-11-293-697-3855	Sequence 3855, Ap
25	221	10.9	128	7	US-11-293-697-4222	Sequence 4222, Ap
26	221	10.9	136	7	US-11-293-697-2898	Sequence 2898, Ap
27	220.5	10.8	111	7	US-11-293-697-2465	Sequence 2465, Ap
28	219	10.8	166	7	US-11-293-697-2532	Sequence 2532, Ap
29	219	10.8	228	7	US-11-293-697-2562	Sequence 2562, Ap
30	217	10.7	104	7	US-11-293-697-2906	Sequence 2906, Ap
31	216	10.6	109	7	US-11-293-697-4725	Sequence 4725, Ap
32	215.5	10.6	101	7	US-11-293-697-4884	Sequence 4884, Ap
33	215.5	10.6	129	7	US-11-293-697-4783	Sequence 4783, Ap
34	209	10.3	108	7	US-11-293-697-4235	Sequence 4235, Ap
35	207	10.2	117	7	US-11-293-697-2879	Sequence 2879, Ap
36	206.5	10.2	101	7	US-11-293-697-2539	Sequence 2539, Ap
37	205.5	10.1	101	7	US-11-293-697-2559	Sequence 2559, Ap
38	201.5	9.9	115	7	US-11-293-697-3605	Sequence 3605, Ap
39	199	9.8	120	7	US-11-293-697-4121	Sequence 4121, Ap
40	198.5	9.8	127	7	US-11-293-697-4007	Sequence 4007, Ap
41	197.5	9.7	113	7	US-11-293-697-3204	Sequence 3204, Ap
42	197	9.7	138	7	US-11-293-697-3556	Sequence 3556, Ap
43	195.5	9.6	106	7	US-11-293-697-4581	Sequence 4581, Ap
44	193	9.5	105	7	US-11-293-697-4709	Sequence 4709, Ap
45	190.5	9.4	100	7	US-11-293-697-3335	Sequence 3335, Ap

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OM protein - protein search, using sw model

Run on: June 5, 2006, 18:24:45 ; Search time 40 Seconds
(without alignments)
902.032 Million cell updates/sec

Title: US-10-092-934-10
Perfect score: 2034
Sequence: 1 MEFSLLLPRLECNGAISAHR.....FIRGGVSPYLSGWSQTPDLR 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	382.5	18.8	673	4	F40201	artifact-warning s
2	315.5	15.5	613	4	C40201	artifact-warning s
3	315.5	15.5	627	4	A40201	artifact-warning s
4	291.5	14.3	597	4	E40201	artifact-warning s
5	197.5	9.7	579	4	D40201	artifact-warning s
6	175	8.6	499	2	S65657	alpha-1C-adrenergi
7	167	8.2	46	2	I54375	gene NF2 protein -
8	161	7.9	841	1	I78885	serine/threonine-s
9	157	7.7	39	2	I54374	gene NF2 protein -
10	151.5	7.4	301	4	B40201	artifact-warning s
11	139.5	6.9	100	2	A46010	X-linked retinopat
12	137.5	6.8	79	2	A56194	thromboxane A-2 re
13	137.5	6.8	407	2	T02670	probable thromboxa
14	128	6.3	53	2	A42442	integrin beta-1 ch
15	112	5.5	440	2	A26359	decay-accelerating
16	106.5	5.2	1125	2	T19193	hypothetical prote
17	105	5.2	522	2	T08711	gamma-adaptin homo
18	102.5	5.0	331	2	S59501	interferon recepto
19	99.5	4.9	331	2	A54295	interferon alpha/b
20	96.5	4.7	1643	1	RRWGNV	genome polyprotein
21	96	4.7	458	2	E82175	conserved hypothet
22	92	4.5	964	2	T15342	hypothetical prote

23	91.5	4.5	542	2	S39608	transcription fact
24	91.5	4.5	631	1	A36749	transcription fact
25	91.5	4.5	1776	1	RRWPYM	genome polyprotein
26	90.5	4.4	282	1	SAVL64	middle surface ant
27	90.5	4.4	832	1	S20752	DNA-directed DNA p
28	90	4.4	431	1	SAVLC2	large surface anti
29	89	4.4	299	2	F84785	probable xylogluca
30	89	4.4	333	2	AI2131	hypothetical prote
31	89	4.4	1162	2	B97852	hypothetical prote
32	88	4.3	209	2	JC4244	heat-shock 27K pro
33	88	4.3	726	2	S18208	rabphilin-3A-inter
34	88	4.3	832	2	S71785	DNA-directed DNA p
35	87.5	4.3	494	2	S39607	transcription fact
36	87	4.3	226	1	JQ1574	major surface anti
37	87	4.3	226	2	JQ2101	surface antigen -
38	87	4.3	470	2	T05258	glycine hydroxymet
39	87	4.3	1153	2	A49676	nitric-oxide synth
40	86.5	4.3	360	2	T45956	hypothetical prote
41	86.5	4.3	1886	2	S04921	nuclear pore prote
42	86	4.2	262	2	AF2291	hypothetical prote
43	86	4.2	625	2	E96721	hypothetical prote
44	85.5	4.2	832	1	JDVLA1	DNA-directed DNA p
45	84.5	4.2	191	2	C72455	hypothetical prote

SCORE Search Results Details for Application 10092934 and Search Result us-10-092-934-10.rup.

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OM protein - protein search, using sw model

Run on: June 5, 2006, 18:21:40 ; Search time 297 Seconds
(without alignments)
1167.949 Million cell updates/sec

Title: US-10-092-934-10
Perfect score: 2034
Sequence: 1 MEFSLLLPRLECNGAISAHR.....FIRGGVSPYLSGWSQTPDLR 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2034	100.0	375	2 O60448_HUMAN	O60448 homo sapien
2	595	29.3	587	1 ALU2_HUMAN	P39189 homo sapien
3	568	27.9	587	1 ALU3_HUMAN	P39190 homo sapien
4	549.5	27.0	591	1 ALU8_HUMAN	P39195 homo sapien
5	498.5	24.5	591	1 ALU1_HUMAN	P39188 homo sapien
6	389	19.1	585	1 ALU5_HUMAN	P39192 homo sapien
7	377.5	18.6	158	2 Q8NAL9_HUMAN	Q8nal9 homo sapien
8	357.5	17.6	593	1 ALU6_HUMAN	P39193 homo sapien
9	356.5	17.5	603	1 ALU4_HUMAN	P39191 homo sapien
10	349	17.2	157	2 Q8N845_HUMAN	Q8n845 homo sapien
11	337.5	16.6	164	2 Q6ZTS0_HUMAN	Q6zts0 homo sapien

12	332	16.3	176	2	Q6ZR92_HUMAN	Q6zr92	homo sapien
13	331	16.3	170	2	Q6ZVI4_HUMAN	Q6zvi4	homo sapien
14	330.5	16.2	593	1	ALU7_HUMAN	P39194	homo sapien
15	325	16.0	143	2	Q6ZSJ7_HUMAN	Q6zsj7	homo sapien
16	320	15.7	195	2	Q6ZUW2_HUMAN	Q6zuw2	homo sapien
17	316	15.5	152	2	Q9NX85_HUMAN	Q9nx85	homo sapien
18	303.5	14.9	239	2	Q6ZWA9_HUMAN	Q6zwa9	homo sapien
19	303	14.9	124	2	Q6ZVF6_HUMAN	Q6zvf6	homo sapien
20	301	14.8	156	2	Q8N266_HUMAN	Q8n266	homo sapien
21	295	14.5	193	2	Q6ZVX8_HUMAN	Q6zvx8	homo sapien
22	294.5	14.5	148	2	Q6ZUC5_HUMAN	Q6zuc5	homo sapien
23	290	14.3	123	2	Q6ZV58_HUMAN	Q6zv58	homo sapien
24	287.5	14.1	166	2	Q6ZUC0_HUMAN	Q6zuc0	homo sapien
25	287	14.1	180	2	Q8N7M7_HUMAN	Q8n7m7	homo sapien
26	286.5	14.1	130	2	Q6ZSV2_HUMAN	Q6zsv2	homo sapien
27	286.5	14.1	131	2	Q6ZTD3_HUMAN	Q6ztd3	homo sapien
28	283	13.9	125	2	Q6ZTE1_HUMAN	Q6zte1	homo sapien
29	281.5	13.8	147	2	Q6ZUA2_HUMAN	Q6zua2	homo sapien
30	280	13.8	165	2	Q6ZTF6_HUMAN	Q6ztf6	homo sapien
31	279.5	13.7	132	2	Q6ZS28_HUMAN	Q6zs28	homo sapien
32	279	13.7	142	2	Q6ZWD5_HUMAN	Q6zwd5	homo sapien
33	277	13.6	145	2	Q4R5J6_MACFA	Q4r5j6	macaca fasc
34	276	13.6	129	2	Q6ZW43_HUMAN	Q6zw43	homo sapien
35	274	13.5	125	2	Q8N8C2_HUMAN	Q8n8c2	homo sapien
36	274	13.5	164	2	Q6ZUK0_HUMAN	Q6zuk0	homo sapien
37	273.5	13.4	118	2	Q9H387_HUMAN	Q9h387	homo sapien
38	272	13.4	140	2	Q6ZU13_HUMAN	Q6zul3	homo sapien
39	271	13.3	121	2	Q6ZQS8_HUMAN	Q6zqs8	homo sapien
40	269	13.2	137	2	Q6ZS97_HUMAN	Q6zs97	homo sapien
41	269	13.2	241	2	Q6ZTY3_HUMAN	Q6zty3	homo sapien
42	268.5	13.2	129	2	Q6ZUW8_HUMAN	Q6zuw8	homo sapien
43	268	13.2	260	2	Q6ZQR8_HUMAN	Q6zqr8	homo sapien
44	267.5	13.2	165	2	Q6ZS53_HUMAN	Q6zs53	homo sapien
45	267.5	13.2	165	2	Q6ZT71_HUMAN	Q6zt71	homo sapien

ALIGNMENTS

RESULT 1

O60448_HUMAN

ID O60448_HUMAN PRELIMINARY; PRT; 375 AA.

AC O60448;

DT 01-AUG-1998, integrated into UniProtKB/TrEMBL.

DT 01-AUG-1998, sequence version 1.

DT 07-FEB-2006, entry version 15.

DE Neuronal thread protein AD7c-NTP.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Neuronal;

RX MEDLINE=98064067; PubMed=9399956;

RA Monte S.M., Ghanbari K., Frey W.H., Beheshti I., Averbach P.,

RA Hauser S.L., Ghanbari H.A., Wands J.R.;

RT "Characterization of the AD7C-NTP cDNA expression in Alzheimer's disease and measurement of a 41-kD protein in cerebrospinal fluid.";

RL J. Clin. Invest. 100:3093-3104(1997).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Neuronal;

RA de la Monte S.M., Wands J.R.;